# Camila Duitama González

Paris.France

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## **Summary**

Python-focused software engineer with advanced expertise in backend development, data engineering, and algorithmic solutions. Proven ability to design, implement, and optimize complex software systems across research and commercial domains.

### Skills\_

**SQL & Database Management** Advanced SQL, MySQL, SQLite

**Data Engineering & Analytics Machine Learning & Data Science**  Apache Spark, Pandas, NumPy, Data Pipeline Development Scikit-learn, PyTorch, TensorFlow, Metaflow, Dask, Predictive Modeling

Python, R, Bash, Docker, Git, Continuous Integration

**Programming & Development Cloud & Infrastructure** 

AWS, High-Performance Computing, Slurm, Singularity, Cloud Workflows

**Data Visualization & Reporting Bioinformatics Tools** 

Jupyter, R Markdown, LaTeX, Plotly, D3.js, Matplotlib Nextflow, Bioconda, Snakemake, GATK, Samtools

Spanish (Native), English (C2), French (B2), German (B1)

# **Experience**

#### Sequence Bioinformatics Group, Institut Pasteur

Paris. France

January 2024 - Present

- POSTDOCTORAL RESEARCHER
- Lead data engineering efforts for large-scale genetic research projects.

Languages

- Develop and optimized data pipelines for genotype-phenotype association studies.
- Implement machine learning models for complex biological data analysis.
- Mentor and supervise a team of computer scientists and programmers.

#### Max Planck Institute for Biology of Ageing

Cologne, Germany

RESEARCH ASSISTANT/PYTHON DEVELOPER

Jan-Dec 2018, Apr-Aug 2020

- Performed dimensionality reduction and multivariate analysis of heterogenous data types.
- Contributed to a Flask-based app for visualisation and analysis of biological data using Python and Docker.

#### **Max Planck Institute of Biochemistry**

Munich, Germany

INTERN

March 2017 - July 2017

• Conducted database curation, statistical analysis, visualization, and reporting for a multidisciplinary group of scientists.

#### Education

#### Sorbonne Université - Institut Pasteur

Paris, France

Ph.D. Information and Communication Science and Technology

October 2020 - January 2023

- · Implemented and created machine learning algorithms for large-scale data classification and analysis.
- Developed predictive models using Python and various ML frameworks (Scikit-learn, Dask).
- · Served as Teaching Assistant, demonstrating ability to convey complex technical concepts to diverse audiences.

**Bonn University** Bonn, Germany

M.Sc. IN LIFE SCIENCE INFORMATICS

Oct 2017 - Oct 2019

• Master thesis: Developed and validated a Bayesian model for risk prediction using R and Python.

· Gained experience in building predictive models and conducting statistical analyses on large datasets.

#### Universidad Nacional de Colombia

Medellín, Colombia

B.Eng. in Biological Engineering

Feb 2012 - Sept 2017

# Open-Source Software Tools \_\_\_\_\_

#### **Unitig Matrix Construction Utility**

MUSET

· Software for constructing abundance unitig matrices from sequencing data.

Open-source repository: github.com/CamilaDuitama/muset

#### **Ancient DNA Decontamination Toolkit**

2023

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2025

• Innovative Python tool for preprocessing and decontaminating ancient DNA samples.

• Open-source repository: github.com/CamilaDuitama/aKmerBroom

#### **Microbial Source Tracking Tool**

2023

DECOM

- High-performance tool for similarity-based microbial source tracking.
- Developed for analyzing microbial composition in ancient oral samples.

• Open-source repository: github.com/CamilaDuitama/decOM

# **Presentations**

**Genome Informatics** Wellcome Genome Campus, UK

PRESENTER FOR "MUSET: SET OF UTILITIES FOR THE CONSTRUCTION OF ABUNDANCE UNITIG MATRICES FROM SEQUENCING

AKMERBROOM

• Speaker in Session 2: Genome Assembly and Sequencing Algorithms

RECOMB-Seq 2023 Istanbul, Turkey

PRESENTER FOR "AKMERBROOM: ANCIENT ORAL DNA DECONTAMINATION USING BLOOM FILTERS ON K-MER SETS"

• Delivered a proceedings talk on novel ancient DNA decontamination techniques.

#### Learning Meaningful Representations for Life (LMRL) Workshop, NeurIPS 2022

Virtual

ACCEPTED PAPER AND POSTER 2022

· Presented research poster in the proceedings track.

## **Publications**

#### **Journal Article**

МІСКОВІОМЕ

 Duitama González, C., Vicedomini, R., Lemane, T., Rascovan, N., Richard, H., & Chikhi, R. (2023). decOM: similarity-based microbial source tracking of ancient oral samples using k-mer-based methods. Microbiome, 11(1), 243.

#### **Journal Article**

**ISCIENCE** 

 González, C. D., Rangavittal, S., Vicedomini, R., Chikhi, R., & Richard, H. (2023). aKmerBroom: Ancient oral DNA decontamination using Bloom filters on k-mer sets. iScience, 26(11).

#### Journal article

OXFORD BIOINFORMATICS 2025

· Vicedomini, R., Andreace, F., Dufresne, Y., Chikhi, R., & Duitama González, C. (under review). MUSET: Set of utilities for the construction of abundance unitig matrices from sequencing data.

## References

Dr. Rayan Chikhi Institut Pasteur, Paris, France

PI AT THE SEQUENCE BIOINFORMATICS GROUP

PhD/Postdoc supervisor

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Robert Koch Institute / Sorbonne University

RESEARCHER / ASSOCIATE PROF. (ON LEAVE)

PhD/Postdoc supervisor

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**Dr. Hugues Richard** 

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**Dr. Ashar Ahmad** ASSOCIATE DIRECTOR, DATA SCIENCE & ADVANCED ANALYTICS Grünenthal Group, Bonn, Germany

Master thesis supervisor

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